

The complete chloroplast genome sequences of potato wild relative species, *Solanum commersonii*

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ABSTRACT

Solanum commersonii Dunal is a well-known wild potato belonging to Solanaceae family and commonly used as materials for somatic hybridization due to various biotic and abiotic stress resistances. The complete chloroplast genome of *S. commersonii* was constituted by *de novo* assembly using a small amount of whole genome sequencing data. The chloroplast genome of *S. commersonii* was 155 525 bp in length, consisted of 86 013 bp of large single copy, 18 366 bp of small single copy region and 25 573 bp of a pair of inverted repeats. A total of 113 genes were annotated including 79 protein-coding genes, 30 tRNA genes and four rRNA genes. Maximum likelihood phylogenetic analysis with 14 Solanaceae species revealed that *S. commersonii* is much closely related to *Solanum tuberosum* and *S. bulbocastanum*.

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Solanum commersonii is a wild diploid potato species, which is native in Uruguay, Argentina and Brazil. It has several desirable characteristics such as disease resistance to bacterial wilt and common scab, and abiotic stress resistance such as cold and frost tolerance (Carputo et al. 2009). Therefore, potato breeders have extensively used *S. commersonii* to make a somatic hybridization and bridge cross in order to introgress useful genetic traits from *S. commersonii* into a cultivated potato (Carputo et al. 1997, 2009, 2013). Somatic hybridization via protoplast fusion provides opportunity to overcome sexual barriers for interspecific gene transfer in potato breeding program (Kim-Lee et al. 2005; Yu, et al. 2013; Zhao et al. 2013). Aversano et al. (2015) reported ~830 Mb of draft genome sequences of *S. commersonii*, of which transposable elements comprise 44.5% of the genome. They also indicated that *S. commersonii* had diverged about ~2.3 million years ago from domesticated potato and three duplication events for enrichment of gene families associated with biotic and abiotic stress resistance (Aversano et al. 2015).

Total genomic DNA was isolated from *S. commersonii* (PI320266) leaves provided by Highland Agriculture Research Institute (HARI), National Institute of Crop Science, Rural Development Administration, Pyeongchang, South Korea. *Solanum commersonii* line (PI320266) was originally introduced from Wisconsin Univ. and maintained in HARI as an *in vitro* plant. An Illumina paired-end (PE) genomic library was constructed according to the PE standard protocol (Illumina, San Diego, CA) and sequenced using an Illumina HiSeq2000 at Macrogen (<http://www.macrogen.com/kor/>),

South Korea. Low-quality bases (Phred score less than 20) were trimmed, and then 3 Gbp of high-quality PE reads were assembled by a CLC genome assembler (ver. 4.06 beta, CLC Inc, Aarhus, Denmark) as described in Kim et al. (2015). The representative chloroplast contigs were extracted and merged into a single draft sequence by comparison with the *Solanum tuberosum* (DQ386163.2) as a reference. The draft chloroplast sequence was further corrected by mapping raw PE reads. The chloroplast genes were predicted using the program DOGMA (Wyman et al. 2004) and BLAST searches.

The complete chloroplast genome of *S. commersonii* (GenBank accession no. KM489054) was 155 525 bp long, and the structure and gene features were typically identical to those of reported higher plants. It consisted of four well-defined regions such as 86,013 bp of large single copy (LSC), 18 366 bp of small single copy region (SSC) and 25 573 bp of a pair of inverted repeats (IRa and IRb). A total of 113 genes were annotated including 79 protein-coding genes, 30 tRNA genes and four rRNA genes. An overall GC content was 37.88%.

Phylogenetic relationship was analyzed using chloroplast coding sequences of *S. commersonii* and 14 published species in Solanaceae by a maximum likelihood method in MEGA 6.0 (Tamura et al. 2013). According to the phylogenetic tree, *S. commersonii* was much closely related to *Solanum tuberosum* and *S. bulbocastanum*, and separated with three tomato species among 14 species in Solanaceae, as expected (Figure 1).

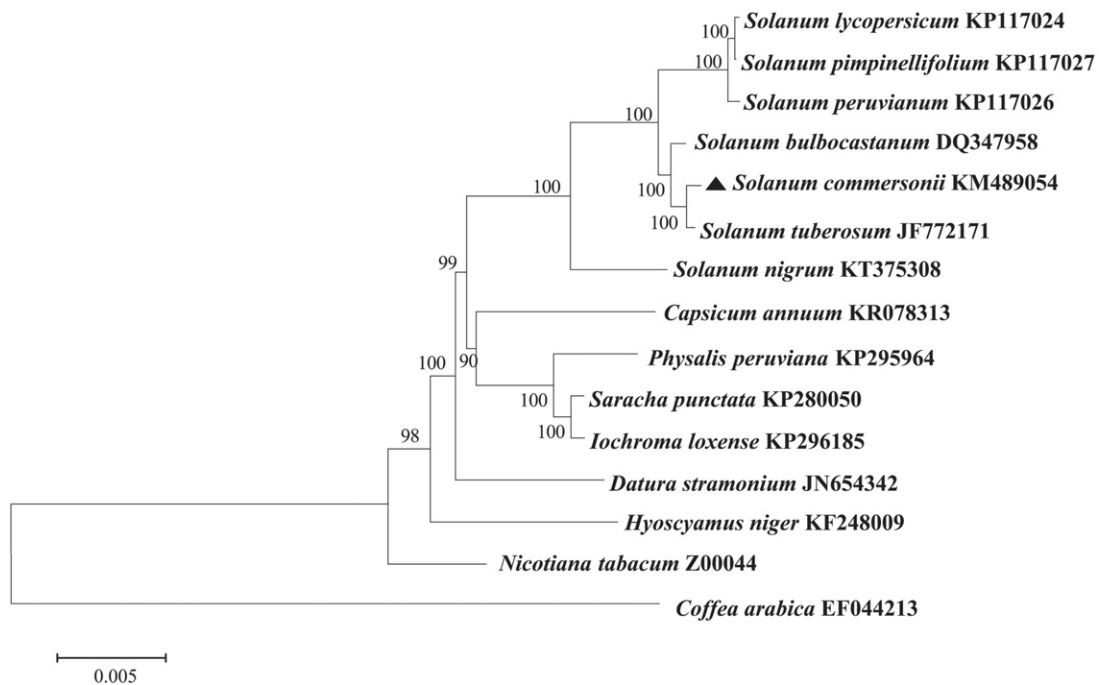


Figure 1. Maximum likelihood phylogenetic tree of *S. commersonii* with 14 species belonging to the Solanaceae based on chloroplast protein coding sequences. Numbers in the nodes are the bootstrap values from 1000 replicates. The chloroplast sequence of *Coffea arabica* was set as an outgroup.

Disclosure statement

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